IN THE SPECIFICATION

Please amend the specification as follows:

At page 3, line 22, please insert:

--**Brief Description of the Drawings**

Figure 1 shows a schema for the bioinformatic analysis of PFI-002 (db = database).

Figure 2 shows the specific functional response of PFI-002 receptor to neuromedin U. The grid corresponds to a 96 well plate and each square of the grid corresponds to one screened peptide (see list of screened peptides under FUNCTIONAL STUDIES section below - e.g. square A1 relates to the result for peptide Arg-Gly-Asp-Ser (RGDS); square B1 relates to the result for peptide [Arg8]Vasopressin, etc.).

Figure 3 shows a ClustalW alignment of PFI-002 with SW|P20789|NTR1_RAT NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1).

Figure 4 shows a ClustalW alignment of PFI-002 with GB|AF044601|NMUR1_Human NEUROMEDIN RECEPTOR TYPE 1 (NMU-R-1).

Figure 5A shows SEQ ID NO: 1, which is the nucleotide sequence coding for PFI-002. The ATG translation initiation codon is indicated by the first three letters. The stop codon is indicated by the last three letters.

Figure 5B shows **SEQ ID NO: 2** shows the corresponding amino acid sequence coding for PFI-002.

Figure 6 shows SEQ ID NOS: 3-6 which are the various primers used throughout the Examples.--.

At page 23, lines 5-13, please rewrite the paragraph as follows:

--As indicated, for some applications, sequence homology (or identity) may be determined using any suitable homology algorithm, using for example default parameters.